



SEQUENCE LISTING

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Rigel Pharmaceuticals, Inc.

<120> Modulators of Cellular Proliferation

<130> 021044-004010US

<140> US 10/620,052

<141> 2003-07-14

<150> US 60/395,443

<151> 2002-07-12

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<170> PatentIn Ver. 2.1

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protein kinase C isoform

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protein kinase C isoform

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 isoform a (PLC-beta1), transcript variant 1

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Gln Glu Lys Leu Val Glu Lys His Lys Glu Ile Arg Gln Gln Ile Leu
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Asp Glu Lys Pro Lys Leu Gln Val Glu Leu Glu Gln Glu Tyr Gln Asp
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Lys Phe Lys Arg Leu Pro Leu Glu Ile Leu Glu Phe Val Gln Glu Ala
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Met Lys Gly Lys Ile Ser Glu Asp Ser Asn His Gly Ser Ala Pro Leu
 1170 1175 1180

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<213> Homo sapiens

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<223> cytoplasmic tyrosine kinase focal adhesion kinase
 (FAK)

<400> 5

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<211> 879

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<223> cytoplasmic tyrosine kinase focal adhesion kinase
(FAK)

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Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys Phe Lys Cys Ala
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85 90 95

Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn Pro Thr His Leu
100 105 110

Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser Asn Ser Glu Asp
115 120 125

Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala Gly Ala Pro Glu
130 135 140

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kinase 2 (FAK2)

<400> 7

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<211> 1009

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<223> calcium dependent tyrosine kinase focal adhesion
kinase 2 (FAK2)

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 Tyr Asp Leu Gln Ile Arg Tyr Leu Pro Glu Asp Phe Met Glu Ser Leu
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 Lys Glu Asp Arg Thr Thr Leu Leu Tyr Phe Tyr Gln Gln Leu Arg Asn
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 Phe Ala Asn Ile Asp Gln Glu Thr Tyr Arg Cys Glu Leu Ile Gln Gly
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 Asp Gly Glu Lys Arg Asn Ser Leu Pro Gln Ile Pro Met Leu Asn Leu
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 770 775 780
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 alpha 1 subunit isoform a, transcript variant 2
 (CK2, CK2alpha), CK2 catalytic subunit alpha

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Cys	Leu	Gln	His	Phe	Tyr	Gly	Pro	Asn	His	Glu	His	Cys	Phe	Asn	Arg	385	390	395
Thr	Leu	Leu	Arg	Asn	Ser	Ser	Gly	Cys	Glu	Ala	Arg	Arg	Asp	Glu	Tyr	405	410	415
Arg	Thr	Glu	Phe	Thr	Thr	Ala	Leu	Gln	Arg	Val	Asp	Leu	Phe	Met	Gly	420	425	430
Gln	Phe	Ser	Glu	Val	Leu	Leu	Thr	Ser	Ile	Ser	Thr	Phe	Ile	Lys	Gly	435	440	445
Asp	Leu	Thr	Ile	Ala	Asn	Leu	Gly	Thr	Ser	Glu	Gly	Arg	Phe	Met	Gln	450	455	460
Val	Val	Val	Ser	Arg	Ser	Gly	Pro	Ser	Thr	Pro	His	Val	Asn	Phe	Leu	465	470	475
Leu	Asp	Ser	His	Pro	Val	Ser	Pro	Glu	Val	Ile	Val	Glu	His	Thr	Leu	485	490	495
Asn	Gln	Asn	Gly	Tyr	Thr	Leu	Val	Ile	Thr	Gly	Lys	Lys	Ile	Thr	Lys	500	505	510
Ile	Pro	Leu	Asn	Gly	Leu	Gly	Cys	Arg	His	Phe	Gln	Ser	Cys	Ser	Gln	515	520	525
Cys	Leu	Ser	Ala	Pro	Pro	Phe	Val	Gln	Cys	Gly	Trp	Cys	His	Asp	Lys	530	535	540
Cys	Val	Arg	Ser	Glu	Glu	Cys	Leu	Ser	Gly	Thr	Trp	Thr	Gln	Gln	Ile	545	550	555
Cys	Leu	Pro	Ala	Ile	Tyr	Lys	Val	Phe	Pro	Asn	Ser	Ala	Pro	Leu	Glu	565	570	575
Gly	Gly	Thr	Arg	Leu	Thr	Ile	Cys	Gly	Trp	Asp	Phe	Gly	Phe	Arg	Arg	580	585	590
Asn	Asn	Lys	Phe	Asp	Leu	Lys	Lys	Thr	Arg	Val	Leu	Leu	Gly	Asn	Glu	595	600	605
Ser	Cys	Thr	Leu	Thr	Leu	Ser	Glu	Ser	Thr	Met	Asn	Thr	Leu	Lys	Cys	610	615	620
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Ser	Asn	Gly	His	Gly	Thr	Thr	Gln	Tyr	Ser	Thr	Phe	Ser	Tyr	Val	Asp	645	650	655
Pro	Val	Ile	Thr	Ser	Ile	Ser	Pro	Lys	Tyr	Gly	Pro	Met	Ala	Gly	Gly	660	665	670
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Ser	Tyr	Arg	Glu	Asp	Pro	Ile	Val	Tyr	Glu	Ile	His	Pro	Thr	Lys	Ser	
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Phe	Ile	Ser	Thr	Trp	Trp	Lys	Glu	Pro	Leu	Asn	Ile	Val	Ser	Phe	Leu	
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Thr Phe Ile Gly Glu His Tyr Val His Val Asn Ala Thr Tyr Val Asn
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<212> DNA

<213> Homo sapiens

<220>

<223> flap structure-specific endonuclease 1 (FEN1)
5'-3' exonuclease

<400> 13

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<211> 380

<212> PRT

<213> Homo sapiens

<220>

<223> flap structure-specific endonuclease 1 (FEN1)

5'-3' exonuclease

<400> 14

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Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
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Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
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Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
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```

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
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Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
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Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
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Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
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 Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala
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 Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg
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 His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His
 195 200 205
 Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val
 210 215 220
 Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly
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 Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile
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 Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu
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 Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val
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 Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg
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<211> 4276

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<213> Homo sapiens

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<223> REV1 dCMP transferase

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taaaatacat	gaaaaggctg	atgcagcaat	cggttgaatc	ggttttggaa	atggcattttg	3900
actttattct	tgacaatgtc	caggtgggtt	tacaacaaac	ttatggaagc	acattaaaag	3960
ttacataaat	attaccagag	agcctgatgc	tctctgatag	ctgtgccata	agtgttctgt	4020

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aggattttgc aaagtgcattg atagtaattgc tcggagtttt tataatttta aattttctttt 4080
aaagcaagtg ttttgtacat ttcttttcaa aaagtgcctaa atttgtcagt attgcatgta 4140
aataattgtg ttaattattt tactgttagca tagattctat ttacaaaatg tttgtttata 4200
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aaaaaaaaa aaaaaa 4276

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<210> 16
<211> 1251
<212> PRT
<213> Homo sapiens

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<220>
<223> REV1 dCMP transferase

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<400> 16
Met Arg Arg Gly Gly Trp Arg Lys Arg Ala Glu Asn Asp Gly Trp Glu
  1              5              10              15

Thr Trp Gly Gly Tyr Met Ala Ala Lys Val Gln Lys Leu Glu Glu Gln
      20              25              30

Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
      35              40              45

Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
      50              55              60

Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
      65              70              75              80

Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
      85              90              95

Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
      100             105             110

Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
      115             120             125

Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
      130             135             140

Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
      145             150             155             160

Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
      165             170             175

Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
      180             185             190

Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
      195             200             205

Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
      210             215             220

Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
      225             230             235             240

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Cys Leu Val Pro Met Val Asn Ser Val Ala Ser Arg Leu Ser Pro Ala
 245 250 255
 Phe Ser Gln Glu Glu Asp Lys Ala Glu Lys Ser Ser Thr Asp Phe Arg
 260 265 270
 Asp Cys Thr Leu Gln Gln Leu Gln Gln Ser Thr Arg Asn Thr Asp Ala
 275 280 285
 Leu Arg Asn Pro His Arg Thr Asn Ser Phe Ser Leu Ser Pro Leu His
 290 295 300
 Ser Asn Thr Lys Ile Asn Gly Ala His His Ser Thr Val Gln Gly Pro
 305 310 315 320
 Ser Ser Thr Lys Ser Thr Ser Ser Val Ser Thr Phe Ser Lys Ala Ala
 325 330 335
 Pro Ser Val Pro Ser Lys Pro Ser Asp Cys Asn Phe Ile Ser Asn Phe
 340 345 350
 Tyr Ser His Ser Arg Leu His His Ile Ser Met Trp Lys Cys Glu Leu
 355 360 365
 Thr Glu Phe Val Asn Thr Leu Gln Arg Gln Ser Asn Gly Ile Phe Pro
 370 375 380
 Gly Arg Glu Lys Leu Lys Lys Met Lys Thr Gly Arg Ser Ala Leu Val
 385 390 395 400
 Val Thr Asp Thr Gly Asp Met Ser Val Leu Asn Ser Pro Arg His Gln
 405 410 415
 Ser Cys Ile Met His Val Asp Met Asp Cys Phe Phe Val Ser Val Gly
 420 425 430
 Ile Arg Asn Arg Pro Asp Leu Lys Gly Lys Pro Val Ala Val Thr Ser
 435 440 445
 Asn Arg Gly Thr Gly Arg Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln
 450 455 460
 Leu Glu Trp Gln Tyr Tyr Gln Asn Lys Ile Leu Lys Gly Lys Ala Ala
 465 470 475 480
 Asp Ile Pro Asp Ser Ser Leu Trp Glu Asn Pro Asp Ser Ala Gln Ala
 485 490 495
 Asn Gly Ile Asp Ser Val Leu Ser Arg Ala Glu Ile Ala Ser Cys Ser
 500 505 510
 Tyr Glu Ala Arg Gln Leu Gly Ile Lys Asn Gly Met Phe Phe Gly His
 515 520 525
 Ala Lys Gln Leu Cys Pro Asn Leu Gln Ala Val Pro Tyr Asp Phe His
 530 535 540
 Ala Tyr Lys Glu Val Ala Gln Thr Leu Tyr Glu Thr Leu Ala Ser Tyr
 545 550 555 560

Thr His Asn Ile Glu Ala Val Ser Cys Asp Glu Ala Leu Val Asp Ile
 565 570 575
 Thr Glu Ile Leu Ala Glu Thr Lys Leu Thr Pro Asp Glu Phe Ala Asn
 580 585 590
 Ala Val Arg Met Glu Ile Lys Asp Gln Thr Lys Cys Ala Ala Ser Val
 595 600 605
 Gly Ile Gly Ser Asn Ile Leu Leu Ala Arg Met Ala Thr Arg Lys Ala
 610 615 620
 Lys Pro Asp Gly Gln Tyr His Leu Lys Pro Glu Glu Val Asp Asp Phe
 625 630 635 640
 Ile Arg Gly Gln Leu Val Thr Asn Leu Pro Gly Val Gly His Ser Met
 645 650 655
 Glu Ser Lys Leu Ala Ser Leu Gly Ile Lys Thr Cys Gly Asp Leu Gln
 660 665 670
 Tyr Met Thr Met Ala Lys Leu Gln Lys Glu Phe Gly Pro Lys Thr Gly
 675 680 685
 Gln Met Leu Tyr Arg Phe Cys Arg Gly Leu Asp Asp Arg Pro Val Arg
 690 695 700
 Thr Glu Lys Glu Arg Lys Ser Val Ser Ala Glu Ile Asn Tyr Gly Ile
 705 710 715 720
 Arg Phe Thr Gln Pro Lys Glu Ala Glu Ala Phe Leu Leu Ser Leu Ser
 725 730 735
 Glu Glu Ile Gln Arg Arg Leu Glu Ala Thr Gly Met Lys Gly Lys Arg
 740 745 750
 Leu Thr Leu Lys Ile Met Val Arg Lys Pro Gly Ala Pro Val Glu Thr
 755 760 765
 Ala Lys Phe Gly Gly His Gly Ile Cys Asp Asn Ile Ala Arg Thr Val
 770 775 780
 Thr Leu Asp Gln Ala Thr Asp Asn Ala Lys Ile Ile Gly Lys Ala Met
 785 790 795 800
 Leu Asn Met Phe His Thr Met Lys Leu Asn Ile Ser Asp Met Arg Gly
 805 810 815
 Val Gly Ile His Val Asn Gln Leu Val Pro Thr Asn Leu Asn Pro Ser
 820 825 830
 Thr Cys Pro Ser Arg Pro Ser Val Gln Ser Ser His Phe Pro Ser Gly
 835 840 845
 Ser Tyr Ser Val Arg Asp Val Phe Gln Val Gln Lys Ala Lys Lys Ser
 850 855 860
 Thr Glu Glu Glu His Lys Glu Val Phe Arg Ala Ala Val Asp Leu Glu
 865 870 875 880

Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys Tyr Met Lys Arg Leu
1205 1210 1215

Met Gln Gln Ser Val Glu Ser Val Trp Asn Met Ala Phe Asp Phe Ile
1220 1225 1230

Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr Tyr Gly Ser Thr Leu
1235 1240 1245

Lys Val Thr
1250

<210> 17
<211> 2957
<212> DNA
<213> Homo sapiens

<220>
<223> apyrimidinic endonuclease 1 (APE1), AP
endonuclease 1, HAP1

<400> 17
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ctccagggac ctgtcttctt aacgtccagg gagcccagac caactcgcgc cttacattcg 120
tatccgtttt cctatctctt tcccgtgggt agcccagcct tctccactgt ttttttcctc 180
ttgcacagag ttagaatctt aagtcagtggt cacacaatgt gctgtgcatc tggcacaacg 240
ataaacagcc gagggagggt tggggactaa gtgcctagag aattagagga gggaggcgag 300
gctaagcgtc cgtcacgtgg tgtcagacag accaatcacg cgcattcttc ggccacgaca 360
agcgcgcctc tgatcacgtg accaggtccg ctaccacagt gggggctcag cgtgcaccct 420
tctttgtgct cgggttagga ggagctaggg tgccatcggg ccggtgcaga tacgggggtg 480
ctcttttgct cataagaggg gcttcgctgg cagtctgaac ggcaagcttg agtcaggacc 540
cttaattaag atcctcaatt ggctggaggg cagatctcgc gagtagggta caaggcacta 600
tgaaatgatc tagtttcgtg ggtgaggggc tgaagggcct atgatgcacg gaggcgggga 660
aaggatttag agataacgtg gtttaaaggc gggacctggt gcggggacgc tccttgggag 720
gagtcttctc ccagccttag ctggtttcat gatctctttg cgtctgtagg caacgcggta 780
aaaatatatg ttcgggtgggt gacgcgggtac agctgccccaa gggcggttcgt aacgggaatg 840
ccgaagcgtg ggaaaaaggg agcgggtggcg gaagacgggg atgagctcag gacaggtaa 900
ggaatgaaat cagcccttct tcctagaagc tgcggcgggg gtgtttgtca ttccttgat 960
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tcagtatata ttactcattt tatagagcca gagggcaaga agagtaagac ggccgcaaag 1140
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aaaacctcac ccagtggcaa acctgccaca ctcaagatct gctcttgga tgtggatggg 1260
cttcgagcct ggattaagaa gaaaggatta gatgtgagtg gaatttgagg gaaagagaca 1320
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ctgttttatt tttctcctgc ccgtagtttt ctgtggggct tccccagctc tgccagttgt 1440
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actaccagct gaacttcagg agctgcctgg actctctcat caatactggt cagctccttc 1980
ggacaaggaa ggtgacagt gcgtgggccc gctttcccgc cagtgccac tcaaagtctc 2040
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aattctctat ctctgcccc cctcttgatt gctttccctt ttcttatagt tttttatgct 2160
aattctgttt catttctata ggcgatgagg agcatgatca ggaaggccgg gtgattgtgg 2220
ctgaatttga ctgcgtttgtg ctggtaacag catatgtacc taatgcaggc cgaggtctgg 2280

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tacgactgga gtaccggcag cgctgggatg aagcctttcg caagttcctg aagggcctgg 2340
cttccccgaaa gccctttgtg ctgtgtggag acctcaatgt ggcacatgaa gaaattgacc 2400
ttcgcaaccc caaggggaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct 2460
tcggggaatt actgcaggct gtgccactgg ctgacagctt taggcacctc tacccaaca 2520
caccctatgc ctacaccttt tggacttata tgatgaatgc tcgatccaag aatgttggtt 2580
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tccgttccaa ggccctcggc agtgatcact gtcctatcac cctataccta gactgtgac 2700
accacccta aatcactttg agcctgggaa ataagcccc tcaactacca ttccttcttt 2760
aaacactctt cagagaaatc tgcattctat ttctcatgta taaaactagg aatcctccaa 2820
ccaggctcct gtgatagagt tcttttaagc ccaagatttt ttatttgagg gttttttgtt 2880
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taaagagcca tagtttc 2957

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<210> 18
<211> 318
<212> PRT
<213> Homo sapiens

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<220>
<223> apyrimidinic endonuclease 1 (APE1), AP
      endonuclease 1, HAP1

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<400> 18
Met Pro Lys Arg Gly Lys Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
  1             5             10             15

Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
      20             25             30

Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
      35             40             45

Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
      50             55             60

Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
      65             70             75             80

Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile Leu Cys Leu Gln Glu
      85             90             95

Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu Pro
      100            105            110

Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly Tyr
      115            120            125

Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser Tyr
      130            135            140

Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val Ala
      145            150            155            160

Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala Gly
      165            170            175

Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala Phe
      180            185            190

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Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu Cys
 195 200 205
 Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro Lys
 210 215 220
 Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Ala Gln Gly Phe
 225 230 235 240
 Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His Leu
 245 250 255
 Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met Asn
 260 265 270
 Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu Ser
 275 280 285
 His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys Ala
 290 295 300
 Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu
 305 310 315

<210> 19
 <211> 1161
 <212> DNA
 <213> Homo sapiens

<220>
 <223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent
 protein kinase

<400> 19
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 cttctgtttc ccaggcagct ctgtggccat ggatatgttc cagaaggtag agaagatcgg 120
 agagggcacc tatgggggtg tgtacaaggc caagaacagg gagacagggc agctgggtggc 180
 cctgaagaag atcagactgg atttgagat ggaggggggtc ccaagcactg ccatcagggg 240
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 caacgagagg aagctctatc tgggtgtttga gttcctcagc caggacctga agaagtacat 360
 ggactccacc ccaggctcag agctccccct gcacctcatc aagagctacc tcttccagct 420
 gctgcagggg gtgagtttct gccactcaca tcgggtcatc caccgagacc tgaagcccca 480
 gaacctgctc atcaatgagt tgggtgccat caagctggct gacttcggcc tggctcgcg 540
 cttcgggggtg cccctgcgca cctacaccca tgaggtggtg aactgtggt atcgcgcccc 600
 cgagattctc ttgggcagca agttctatac cacagctgtg gatattctga gcattgggtg 660
 catctttgca gagatgggtga ctcgaaaagc cctgtttcct ggtgactctg agattgacca 720
 gctctttcgt atctttcgta tgcctggggac accagcgaa gacacatggc ccgggggtcac 780
 ccagctgcct gactataagg gcagcttccc taagtggacc aggaagggac tgggaagagat 840
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 cactcagatc ctttctcgag cagcagctgc tgccccagct gcctcctacc cattgccaa 1080
 agaggatgca tctggggaga gcaaagcact aaggaattca gcacagcct gcagaggggt 1140
 gagtctgggt tagtctctgcc c 1161

<210> 20
 <211> 305
 <212> PRT
 <213> Homo sapiens

<220>

<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent
protein kinase

<400> 20

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Met Asp Met Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
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Val Val Tyr Lys Ala Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu
      20              25              30

Lys Lys Ile Arg Leu Asp Leu Glu Met Glu Gly Val Pro Ser Thr Ala
      35              40              45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Lys His Pro Asn Ile Val
      50              55              60

Arg Leu Leu Asp Val Val His Asn Glu Arg Lys Leu Tyr Leu Val Phe
      65              70              75              80

Glu Phe Leu Ser Gln Asp Leu Lys Lys Tyr Met Asp Ser Thr Pro Gly
      85              90              95

Ser Glu Leu Pro Leu His Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
      100             105             110

Gln Gly Val Ser Phe Cys His Ser His Arg Val Ile His Arg Asp Leu
      115             120             125

Lys Pro Gln Asn Leu Leu Ile Asn Glu Leu Gly Ala Ile Lys Leu Ala
      130             135             140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Thr Tyr Thr
      145             150             155             160

His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
      165             170             175

Ser Lys Phe Tyr Thr Thr Ala Val Asp Ile Trp Ser Ile Gly Cys Ile
      180             185             190

Phe Ala Glu Met Val Thr Arg Lys Ala Leu Phe Pro Gly Asp Ser Glu
      195             200             205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Met Leu Gly Thr Pro Ser Glu
      210             215             220

Asp Thr Trp Pro Gly Val Thr Gln Leu Pro Asp Tyr Lys Gly Ser Phe
      225             230             235             240

Pro Lys Trp Thr Arg Lys Gly Leu Glu Glu Ile Val Pro Asn Leu Glu
      245             250             255

Pro Glu Gly Arg Asp Leu Leu Met Gln Leu Leu Gln Tyr Asp Pro Ser
      260             265             270

Gln Arg Ile Thr Ala Lys Thr Ala Leu Ala His Pro Tyr Phe Ser Ser
      275             280             285
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Pro Glu Pro Ser Pro Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg
 290 295 300

His
 305

<210> 21
 <211> 2297
 <212> DNA
 <213> Homo sapiens

<220>
 <223> PIM1 oncogene serine threonine kinase

<220>
 <221> modified_base
 <222> (1896)..(1906)
 <223> n = g, a, c or t

<400> 21
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 cctggagtcg cagtaccagg tgggcccgcg actgggcagc ggcggttcg gctcgggtcta 180
 ctcaggcatc cgcgtctccg acaacttgcc ggtggccatc aaacacgtgg agaaggaccg 240
 gatttccgac tggggagagc tgcctaattg cactcgagtg cccatggaag tggtcctgct 300
 gaagaagggt agctcgggtt tctccggcgt cattaggctc ctggactggg tcgagaggcc 360
 cgacagtttc gtcctgatcc tggagaggcc cgagccggtg caagatctct tcgacttcat 420
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 ccttatcgac ctcaatcgcg gcgagctcaa gctcatcgac ttcgggtcgg gggcgctgct 600
 caaggacacc gtctacacgg acttcgatgg gacccgagtg tatagccctc cagagtggat 660
 ccgctaccat cgctaccatg gcaggtcggc ggcagtctgg tccctgggga tcctgctgta 720
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 ggaacaacat ttacaactca ttccagatcc caggcccttg gaggctgcct cccaacagtg 1140
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 cacctcttcc gactctttct gagtgccttc tgtggggact ccggctgtgc tgggagaaat 1440
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<210> 22
 <211> 313
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PIM1 oncogene serine threonine kinase

<400> 22
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 20 25 30
 Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
 35 40 45
 Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
 50 55 60
 Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
 65 70 75 80
 Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
 85 90 95
 Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
 100 105 110
 Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
 115 120 125
 Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
 130 135 140
 Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
 145 150 155 160
 Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
 165 170 175
 Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
 180 185 190
 Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
 195 200 205
 Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
 210 215 220
 Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
 225 230 235 240
 Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
 245 250 255
 Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
 260 265 270

Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
 275 280 285

Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
 290 295 300

His Ser Leu Ser Pro Gly Pro Ser Lys
 305 310

<210> 23
 <211> 3178
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
 division cycle 7-like 1 (CDC7L1) protein serine
 threonine kinase

<400> 23
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<210> 24
<211> 574
<212> PRT
<213> Homo sapiens

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<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
      division cycle 7-like 1 (CDC7L1) protein serine
      threonine kinase

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Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
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Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
 35             40             45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
 50             55             60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
 65             70             75             80

Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
 85             90             95

His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
100             105             110

Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
115             120             125

His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
130             135             140

Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
145             150             155             160

Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
165             170             175

Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
180             185             190

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Ala	Leu	Val	Asp	Phe	Gly	Leu	Ala	Gln	Gly	Thr	His	Asp	Thr	Lys	Ile	195	200	205
Glu	Leu	Leu	Lys	Phe	Val	Gln	Ser	Glu	Ala	Gln	Gln	Glu	Arg	Cys	Ser	210	215	220
Gln	Asn	Lys	Ser	His	Ile	Ile	Thr	Gly	Asn	Lys	Ile	Pro	Leu	Ser	Gly	225	230	235
Pro	Val	Pro	Lys	Glu	Leu	Asp	Gln	Gln	Ser	Thr	Thr	Lys	Ala	Ser	Val	245	250	255
Lys	Arg	Pro	Tyr	Thr	Asn	Ala	Gln	Ile	Gln	Ile	Lys	Gln	Gly	Lys	Asp	260	265	270
Gly	Lys	Glu	Gly	Ser	Val	Gly	Leu	Ser	Val	Gln	Arg	Ser	Val	Phe	Gly	275	280	285
Glu	Arg	Asn	Phe	Asn	Ile	His	Ser	Ser	Ile	Ser	His	Glu	Ser	Pro	Ala	290	295	300
Val	Lys	Leu	Met	Lys	Gln	Ser	Lys	Thr	Val	Asp	Val	Leu	Ser	Arg	Lys	305	310	315
Leu	Ala	Thr	Lys	Lys	Lys	Ala	Ile	Ser	Thr	Lys	Val	Met	Asn	Ser	Ala	325	330	335
Val	Met	Arg	Lys	Thr	Ala	Ser	Ser	Cys	Pro	Ala	Ser	Leu	Thr	Cys	Asp	340	345	350
Cys	Tyr	Ala	Thr	Asp	Lys	Val	Cys	Ser	Ile	Cys	Leu	Ser	Arg	Arg	Gln	355	360	365
Gln	Val	Ala	Pro	Arg	Ala	Gly	Thr	Pro	Gly	Phe	Arg	Ala	Pro	Glu	Val	370	375	380
Leu	Thr	Lys	Cys	Pro	Asn	Gln	Thr	Thr	Ala	Ile	Asp	Met	Trp	Ser	Ala	385	390	395
Gly	Val	Ile	Phe	Leu	Ser	Leu	Leu	Ser	Gly	Arg	Tyr	Pro	Phe	Tyr	Lys	405	410	415
Ala	Ser	Asp	Asp	Leu	Thr	Ala	Leu	Ala	Gln	Ile	Met	Thr	Ile	Arg	Gly	420	425	430
Ser	Arg	Glu	Thr	Ile	Gln	Ala	Ala	Lys	Thr	Phe	Gly	Lys	Ser	Ile	Leu	435	440	445
Cys	Ser	Lys	Glu	Val	Pro	Ala	Gln	Asp	Leu	Arg	Lys	Leu	Cys	Glu	Arg	450	455	460
Leu	Arg	Gly	Met	Asp	Ser	Ser	Thr	Pro	Lys	Leu	Thr	Ser	Asp	Ile	Gln	465	470	475
Gly	His	Ala	Ser	His	Gln	Pro	Ala	Ile	Ser	Glu	Lys	Thr	Asp	His	Lys	485	490	495
Ala	Ser	Cys	Leu	Val	Gln	Thr	Pro	Pro	Gly	Gln	Tyr	Ser	Gly	Asn	Ser	500	505	510

Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe Asp Glu Tyr
515 520 525

Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu Ala Tyr Asp
530 535 540

Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg Ile Thr Ala
545 550 555 560

Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser Leu
565 570

<210> 25

<211> 1427

<212> DNA

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 25

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ttatgagaag ctggacttcc ttggggaggg acagtttgcc accgtttaca aggccagaga 180
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taaagatggg ataaatagaa ccgccttaag agagataaaa ttattacagg agctaagtca 300
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<210> 26

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 26

Met Ala Leu Asp Val Lys Ser Arg Ala Lys Arg Tyr Glu Lys Leu Asp
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Phe Leu Gly Glu Gly Gln Phe Ala Thr Val Tyr Lys Ala Arg Asp Lys
20 25 30

Asn Thr Asn Gln Ile Val Ala Ile Lys Lys Ile Lys Leu Gly His Arg
35 40 45

Ser Glu Ala Lys Asp Gly Ile Asn Arg Thr Ala Leu Arg Glu Ile Lys
50 55 60

Leu Leu Gln Glu Leu Ser His Pro Asn Ile Ile Gly Leu Leu Asp Ala
65 70 75 80

Phe Gly His Lys Ser Asn Ile Ser Leu Val Phe Asp Phe Met Glu Thr
85 90 95

Asp Leu Glu Val Ile Ile Lys Asp Asn Ser Leu Val Leu Thr Pro Ser
100 105 110

His Ile Lys Ala Tyr Met Leu Met Thr Leu Gln Gly Leu Glu Tyr Leu
115 120 125

His Gln His Trp Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu Leu
130 135 140

Leu Asp Glu Asn Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys
145 150 155 160

Ser Phe Gly Ser Pro Asn Arg Ala Tyr Thr His Gln Val Val Thr Arg
165 170 175

Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg Met Tyr Gly Val
180 185 190

Gly Val Asp Met Trp Ala Val Gly Cys Ile Leu Ala Glu Leu Leu Leu
195 200 205

Arg Val Pro Phe Leu Pro Gly Asp Ser Asp Leu Asp Gln Leu Thr Arg
210 215 220

Ile Phe Glu Thr Leu Gly Thr Pro Thr Glu Glu Gln Trp Pro Asp Met
225 230 235 240

Cys Ser Leu Pro Asp Tyr Val Thr Phe Lys Ser Phe Pro Gly Ile Pro
245 250 255

Leu His His Ile Phe Ser Ala Ala Gly Asp Asp Leu Leu Asp Leu Ile
260 265 270

Gln Gly Leu Phe Leu Phe Asn Pro Cys Ala Arg Ile Thr Ala Thr Gln
275 280 285

Ala Leu Lys Met Lys Tyr Phe Ser Asn Arg Pro Gly Pro Thr Pro Gly
290 295 300

Cys Gln Leu Pro Arg Pro Asn Cys Pro Val Glu Thr Leu Lys Glu Gln
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Ser Asn Pro Ala Leu Ala Ile Lys Arg Lys Arg Thr Glu Ala Leu Glu
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Gln Gly Gly Leu Pro Lys Lys Leu Ile Phe
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<210> 27
<211> 2169
<212> DNA
<213> Homo sapiens

<220>
<223> cytokine-inducible kinase (CNK) serine threonine
kinase, proliferation-related kinase (PRK),
polo-like kinase 3 (PLK3)

<400> 27
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<210> 28
<211> 607
<212> PRT
<213> Homo sapiens

<220>

<223> cytokine-inducible kinase (CNK) serine threonine
kinase, proliferation-related kinase (PRK),
polo-like kinase 3 (PLK3)

<400> 28

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Pro	Arg	Ser	Gly	Arg	Thr	Tyr	Leu	Lys	Gly	Arg	Leu	Leu	Gly	Lys	Gly
			20					25					30		
Gly	Phe	Ala	Arg	Cys	Tyr	Glu	Ala	Thr	Asp	Thr	Glu	Thr	Gly	Ser	Ala
		35					40					45			
Tyr	Ala	Val	Lys	Val	Ile	Pro	Gln	Ser	Arg	Val	Ala	Lys	Pro	His	Gln
	50					55					60				
Arg	Glu	Lys	Ile	Leu	Asn	Glu	Ile	Glu	Leu	His	Arg	Asp	Leu	Gln	His
65					70					75					80
Arg	His	Ile	Val	Arg	Phe	Ser	His	His	Phe	Glu	Asp	Ala	Asp	Asn	Ile
				85					90					95	
Tyr	Ile	Phe	Leu	Glu	Leu	Cys	Ser	Arg	Lys	Ser	Leu	Ala	His	Ile	Trp
			100					105					110		
Lys	Ala	Arg	His	Thr	Leu	Leu	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg
		115					120					125			
Gln	Ile	Leu	Ser	Gly	Leu	Lys	Tyr	Leu	His	Gln	Arg	Gly	Ile	Leu	His
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Arg	Asp	Leu	Lys	Leu	Gly	Asn	Phe	Phe	Ile	Thr	Glu	Asn	Met	Glu	Leu
145					150					155					160
Lys	Val	Gly	Asp	Phe	Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Pro	Glu	Gln
				165					170					175	
Arg	Lys	Lys	Thr	Ile	Cys	Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val
			180					185					190		
Leu	Leu	Arg	Gln	Gly	His	Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Leu	Gly
		195					200					205			
Cys	Val	Met	Tyr	Thr	Leu	Leu	Cys	Gly	Ser	Pro	Pro	Phe	Glu	Thr	Ala
	210					215					220				
Asp	Leu	Lys	Glu	Thr	Tyr	Arg	Cys	Ile	Lys	Gln	Val	His	Tyr	Thr	Leu
225					230					235					240
Pro	Ala	Ser	Leu	Ser	Leu	Pro	Ala	Arg	Gln	Leu	Leu	Ala	Ala	Ile	Leu
				245					250					255	
Arg	Ala	Ser	Pro	Arg	Asp	Arg	Pro	Ser	Ile	Asp	Gln	Ile	Leu	Arg	His
			260					265					270		
Asp	Phe	Phe	Thr	Lys	Gly	Tyr	Thr	Pro	Asp	Arg	Leu	Pro	Ile	Ser	Ser
		275					280					285			

Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
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 Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
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 325 330 335
 Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
 340 345 350
 Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
 355 360 365
 Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
 370 375 380
 Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
 385 390 395 400
 Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
 405 410 415
 Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
 420 425 430
 Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
 435 440 445
 Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
 450 455 460
 Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
 465 470 475 480
 Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
 485 490 495
 Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
 500 505 510
 Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val
 515 520 525
 Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
 530 535 540
 Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
 545 550 555 560
 Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
 565 570 575
 Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
 580 585 590
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 595 600 605

<210> 29
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<220>
 <223> potentially prenylated protein tyrosine
 phosphatase (PRL-3), protein tyrosine phosphatase
 type IVA, member 3, isoform 2, transcript variant
 2 (PTP4A3)

<400> 29
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<210> 30
 <211> 148
 <212> PRT
 <213> Homo sapiens

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 <223> potentially prenylated protein tyrosine
 phosphatase (PRL-3), protein tyrosine phosphatase
 type IVA, member 3, isoform 2, transcript variant
 2 (PTP4A3)

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 20 25 30
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 35 40 45
 Cys Glu Val Thr Tyr Asp Lys Thr Pro Leu Glu Lys Asp Gly Ile Thr
 50 55 60

Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val
65 70 75 80

Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro
85 90 95

Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Lys Arg
100 105 110

Arg Gly Ala Ile Asn Ser Lys Gln Leu Thr Tyr Leu Glu Lys Tyr Arg
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Pro Lys Gln Arg Leu Arg Phe Lys Asp Pro His Thr His Lys Thr Arg
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Cys Cys Val Met
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<210> 31
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<212> DNA
<213> Homo sapiens

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<210> 32

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> serine threonine kinase 2 (STK2, NEK4)

<400> 32

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          20                      25          30

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Val Ile Lys Lys Leu Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg
          35                      40          45

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Ala Ala Glu Gln Glu Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn
          50                      55          60

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Ile Val Thr Tyr Lys Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr
          65                      70          75          80

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Ile Val Met Gly Phe Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys
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Glu Gln Lys Gly Gln Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe
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His	Arg	Asp	Leu	Lys	Thr	Gln	Asn	Val	Phe	Leu	Thr	Arg	Thr	Asn	Ile	130	135	140
Ile	Lys	Val	Gly	Asp	Leu	Gly	Ile	Ala	Arg	Val	Leu	Glu	Asn	His	Cys	145	150	155
Asp	Met	Ala	Ser	Thr	Leu	Ile	Gly	Thr	Pro	Tyr	Tyr	Met	Ser	Pro	Glu	165	170	175
Leu	Phe	Ser	Asn	Lys	Pro	Tyr	Asn	Tyr	Lys	Ser	Asp	Val	Trp	Ala	Leu	180	185	190
Gly	Cys	Cys	Val	Tyr	Glu	Met	Ala	Thr	Leu	Lys	His	Ala	Phe	Asn	Ala	195	200	205
Lys	Asp	Met	Asn	Ser	Leu	Val	Tyr	Arg	Ile	Ile	Glu	Gly	Lys	Leu	Pro	210	215	220
Pro	Met	Pro	Arg	Asp	Tyr	Ser	Pro	Glu	Leu	Ala	Glu	Leu	Ile	Arg	Thr	225	230	235
Met	Leu	Ser	Lys	Arg	Pro	Glu	Glu	Arg	Pro	Ser	Val	Arg	Ser	Ile	Leu	245	250	255
Arg	Gln	Pro	Tyr	Ile	Lys	Arg	Gln	Ile	Ser	Phe	Phe	Leu	Glu	Ala	Thr	260	265	270
Lys	Ile	Lys	Thr	Ser	Lys	Asn	Asn	Ile	Lys	Asn	Gly	Asp	Ser	Gln	Ser	275	280	285
Lys	Pro	Phe	Ala	Thr	Val	Val	Ser	Gly	Glu	Ala	Glu	Ser	Asn	His	Glu	290	295	300
Val	Ile	His	Pro	Gln	Pro	Leu	Ser	Ser	Glu	Gly	Ser	Gln	Thr	Tyr	Ile	305	310	315
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Leu	Ser	Asn	Thr	Thr	Glu	Leu	Ala	Thr	Ile	Ser	Ser	Val	Asn	Ile	Asp	355	360	365
Ile	Leu	Pro	Ala	Lys	Gly	Arg	Asp	Ser	Val	Ser	Asp	Gly	Phe	Val	Gln	370	375	380
Glu	Asn	Gln	Pro	Arg	Tyr	Leu	Asp	Ala	Ser	Asn	Glu	Leu	Gly	Gly	Ile	385	390	395
Cys	Ser	Ile	Ser	Gln	Val	Glu	Glu	Glu	Met	Leu	Gln	Asp	Asn	Thr	Lys	405	410	415
Ser	Ser	Ala	Gln	Pro	Glu	Asn	Leu	Ile	Pro	Met	Trp	Ser	Ser	Asp	Ile	420	425	430

Val Thr Gly Glu Lys Asn Glu Pro Val Lys Pro Leu Gln Pro Leu Ile
435 440 445
Lys Glu Gln Lys Pro Lys Asp Gln Ser Leu Ala Leu Ser Pro Lys Leu
450 455 460
Glu Cys Ser Gly Thr Ile Leu Ala His Ser Asn Leu Arg Leu Leu Gly
465 470 475 480
Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Ile Thr Gly
485 490 495
Val Cys His His Ala Gln Asp Gln Val Ala Gly Glu Cys Ile Ile Glu
500 505 510
Lys Gln Gly Arg Ile His Pro Asp Leu Gln Pro His Asn Ser Gly Ser
515 520 525
Glu Pro Ser Leu Ser Arg Gln Arg Arg Gln Lys Arg Arg Glu Gln Thr
530 535 540
Glu His Arg Gly Glu Lys Arg Gln Val Arg Arg Asp Leu Phe Ala Phe
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Gln Glu Ser Pro Pro Arg Phe Leu Pro Ser His Pro Ile Val Gly Lys
565 570 575
Val Asp Val Thr Ser Thr Gln Lys Glu Ala Glu Asn Gln Arg Arg Val
580 585 590
Val Thr Gly Ser Val Ser Ser Ser Arg Ser Ser Glu Met Ser Ser Ser
595 600 605
Lys Asp Arg Pro Leu Ser Ala Arg Glu Arg Arg Arg Leu Lys Gln Ser
610 615 620
Gln Glu Glu Met Ser Ser Ser Gly Pro Ser Val Arg Lys Ala Ser Leu
625 630 635 640
Ser Val Ala Gly Pro Gly Lys Pro Gln Glu Glu Asp Gln Pro Leu Pro
645 650 655
Ala Arg Arg Leu Ser Ser Asp Cys Ser Val Thr Gln Glu Arg Lys Gln
660 665 670
Ile His Cys Leu Ser Glu Asp Glu Leu Ser Ser Ser Thr Ser Ser Thr
675 680 685
Asp Lys Ser Asp Gly Asp Tyr Gly Glu Gly Lys Gly Gln Thr Asn Glu
690 695 700
Ile Asn Ala Leu Val Gln Leu Met Thr Gln Thr Leu Lys Leu Asp Ser
705 710 715 720
Lys Glu Ser Cys Glu Asp Val Pro Val Ala Asn Pro Val Ser Glu Phe
725 730 735
Lys Leu His Arg Lys Tyr Arg Asp Thr Leu Ile Leu His Gly Lys Val
740 745 750

Ala Glu Glu Ala Glu Glu Ile His Phe Lys Glu Leu Pro Ser Ala Ile
755 760 765

Met Pro Gly Ser Glu Lys Ile Arg Arg Leu Val Glu Val Leu Arg Thr
770 775 780

Asp Val Ile Arg Gly Leu Gly Val Gln Leu Leu Glu Gln Val Tyr Asp
785 790 795 800

Leu Leu Glu Glu Glu Asp Glu Phe Asp Arg Glu Val Arg Leu Arg Glu
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His Met Gly Glu Lys Tyr Thr Thr Tyr Ser Val Lys Ala Arg Gln Leu
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Lys Phe Phe Glu Glu Asn Met Asn Phe
835 840

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<211> 1513
<212> DNA
<213> Homo sapiens

<220>
<223> serine threonine protein kinase NKIAMRE,
mitogen-activated protein kinase/cyclin-dependent
kinase-related protein kinase NKIATRE homologue

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 mitogen-activated protein kinase/cyclin-dependent
 kinase-related protein kinase NKIATRE homologue

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 Arg Glu Ile Lys Phe Leu Lys Gln Phe His His Glu Asn Leu Val Asn
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 Phe Ile Asp His Thr Val Leu Asp Glu Leu Gln His Tyr Cys His Gly
 85 90 95
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 Ile Asp Tyr Leu His Ser Asn Asn Ile Ile His Arg Asp Ile Lys Pro
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 Glu Met Ala Thr Gly Asn Pro Tyr Leu Pro Ser Ser Ser Asp Leu Asp
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 Gln Asn Ile Phe Ser Lys Ser Pro Ile Phe Ala Gly Val Val Leu Pro
 225 230 235 240
 Gln Val Gln His Pro Lys Asn Ala Arg Lys Lys Tyr Pro Lys Leu Asn
 245 250 255
 Gly Leu Leu Ala Asp Ile Val His Ala Cys Leu Gln Ile Asp Pro Ala
 260 265 270

Asp Arg Ile Ser Ser Ser Asp Leu Leu His His Glu Tyr Phe Thr Arg
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 Asp Gly Phe Ile Glu Lys Phe Met Pro Glu Leu Lys Ala Lys Leu Leu
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 Glu Asn Glu Leu Arg Lys Asp Glu Arg Lys Thr Val Tyr Thr Asn Thr
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 Gly Leu Lys Glu Asn Pro His Cys Gly Gly Ser Val Thr Met Pro Pro
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 acetyltransferase 2 (MYST2)

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tactggaagg gaaaacacct agtttttaaag agacaggacc tgattgatga gtggatagcc 1800
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cctccaagg gcacttaaag tgacctgtca ttccgagcca gcgaacccca gcagtaggaa 1920
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tcatctctgt acactactta tattcactgt ggggtggggg agctaatttt aagcatgttc 3300
agtggcagct cccctccagt ttcagtgtca ctgttaaaat ttatcaaaaa gcaacttcac 3360
taggggtttt cttaagggat aaaggccttt tacagaagct aaacccttcc ccacatgtgg 3420
tagaatgtgc tcttctatat ctactcctca ataaagcatg ttctctgctc aaaaaaaaaa 3480
aaaaaaaaaa aaaaaaaaaa aaaa 3504

```

<210> 36

<211> 611

<212> PRT

<213> Homo sapiens

<220>

<223> HBO1 histone acetyltransferase, MYST histone
acetyltransferase 2 (MYST2)

<400> 36

Met Pro Arg Arg Lys Arg Asn Ala Gly Ser Ser Ser Asp Gly Thr Glu
1 5 10 15

Asp Ser Asp Phe Ser Thr Asp Leu Glu His Thr Asp Ser Ser Glu Ser
 20 25 30
 Asp Gly Thr Ser Arg Arg Ser Ala Arg Val Thr Arg Ser Ser Ala Arg
 35 40 45
 Leu Ser Gln Ser Ser Gln Asp Ser Ser Pro Val Arg Asn Leu Gln Ser
 50 55 60
 Phe Gly Thr Glu Glu Pro Ala Tyr Ser Thr Arg Arg Val Thr Arg Ser
 65 70 75 80
 Gln Gln Gln Pro Thr Pro Val Thr Pro Lys Lys Tyr Pro Leu Arg Gln
 85 90 95
 Thr Arg Ser Ser Gly Ser Glu Thr Glu Gln Val Val Asp Phe Ser Asp
 100 105 110
 Arg Glu Thr Lys Asn Thr Ala Asp His Asp Glu Ser Pro Pro Arg Thr
 115 120 125
 Pro Thr Gly Asn Ala Pro Ser Ser Glu Ser Asp Ile Asp Ile Ser Ser
 130 135 140
 Pro Asn Val Ser His Asp Glu Ser Ile Ala Lys Asp Met Ser Leu Lys
 145 150 155 160
 Asp Ser Gly Ser Asp Leu Ser His Arg Pro Lys Arg Arg Arg Phe His
 165 170 175
 Glu Ser Tyr Asn Phe Asn Met Lys Cys Pro Thr Pro Gly Cys Asn Ser
 180 185 190
 Leu Gly His Leu Thr Gly Lys His Glu Arg His Phe Ser Ile Ser Gly
 195 200 205
 Cys Pro Leu Tyr His Asn Leu Ser Ala Asp Glu Cys Lys Val Arg Ala
 210 215 220
 Gln Ser Arg Asp Lys Gln Ile Glu Glu Arg Met Leu Ser His Arg Gln
 225 230 235 240
 Asp Asp Asn Asn Arg His Ala Thr Arg His Gln Ala Pro Thr Glu Arg
 245 250 255
 Gln Leu Arg Tyr Lys Glu Lys Val Ala Glu Leu Arg Lys Lys Arg Asn
 260 265 270
 Ser Gly Leu Ser Lys Glu Gln Lys Glu Lys Tyr Met Glu His Arg Gln
 275 280 285
 Thr Tyr Gly Asn Thr Arg Glu Pro Leu Leu Glu Asn Leu Thr Ser Glu
 290 295 300
 Tyr Asp Leu Asp Leu Phe Arg Arg Ala Gln Ala Arg Ala Ser Glu Asp
 305 310 315 320
 Leu Glu Lys Leu Arg Leu Gln Gly Gln Ile Thr Glu Gly Ser Asn Met
 325 330 335

Ile	Lys	Thr	Ile	Ala	Phe	Gly	Arg	Tyr	Glu	Leu	Asp	Thr	Trp	Tyr	His	340	345	350	
Ser	Pro	Tyr	Pro	Glu	Glu	Tyr	Ala	Arg	Leu	Gly	Arg	Leu	Tyr	Met	Cys	355	360	365	
Glu	Phe	Cys	Leu	Lys	Tyr	Met	Lys	Ser	Gln	Thr	Ile	Leu	Arg	Arg	His	370	375	380	
Met	Ala	Lys	Cys	Val	Trp	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	385	390	395	400
Lys	Gly	Ser	Ile	Ser	Val	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Ile	405	410	415	
Tyr	Cys	Gln	Asn	Leu	Cys	Leu	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	420	425	430	
Thr	Leu	Tyr	Tyr	Asp	Val	Glu	Pro	Phe	Leu	Phe	Tyr	Val	Met	Thr	Glu	435	440	445	
Ala	Asp	Asn	Thr	Gly	Cys	His	Leu	Ile	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	450	455	460	
Asn	Ser	Phe	Leu	Asn	Tyr	Asn	Val	Ser	Cys	Ile	Leu	Thr	Met	Pro	Gln	465	470	475	480
Tyr	Met	Arg	Gln	Gly	Tyr	Gly	Lys	Met	Leu	Ile	Asp	Phe	Ser	Tyr	Leu	485	490	495	
Leu	Ser	Lys	Val	Glu	Glu	Lys	Val	Gly	Ser	Pro	Glu	Arg	Pro	Leu	Ser	500	505	510	
Asp	Leu	Gly	Leu	Ile	Ser	Tyr	Arg	Ser	Tyr	Trp	Lys	Glu	Val	Leu	Leu	515	520	525	
Arg	Tyr	Leu	His	Asn	Phe	Gln	Gly	Lys	Glu	Ile	Ser	Ile	Lys	Glu	Ile	530	535	540	
Ser	Gln	Glu	Thr	Ala	Val	Asn	Pro	Val	Asp	Ile	Val	Ser	Thr	Leu	Gln	545	550	555	560
Ala	Leu	Gln	Met	Leu	Lys	Tyr	Trp	Lys	Gly	Lys	His	Leu	Val	Leu	Lys	565	570	575	
Arg	Gln	Asp	Leu	Ile	Asp	Glu	Trp	Ile	Ala	Lys	Glu	Ala	Lys	Arg	Ser	580	585	590	
Asn	Ser	Asn	Lys	Thr	Met	Asp	Pro	Ser	Cys	Leu	Lys	Trp	Thr	Pro	Pro	595	600	605	
Lys	Gly	Thr														610			

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CK2-specific
 siRNA molecule

<400> 37
 aacattgaat tagatccacg t 21

<210> 38
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PIM1-specific
 siRNA molecule

<400> 38
 aaaactccga gtgaactggt c 21

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:HBO1-specific
 siRNA molecule

<400> 39
 aactgagcaa gtggttgatt t 21

<210> 40
 <211> 409
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
 division cycle 7-like 1 (CDC7L1) protein serine
 threonine kinase

<400> 40
 Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
 1 5 10 15
 Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
 20 25 30
 Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
 35 40 45
 Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
 50 55 60
 Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
 65 70 75 80

Val	Gly	Pro	Glu	Glu	Lys	Ile	Ala	Leu	Lys	His	Leu	Ile	Pro	Thr	Ser	
				85					90					95		
His	Pro	Ile	Arg	Ile	Ala	Ala	Glu	Leu	Gln	Cys	Leu	Thr	Val	Ala	Gly	
			100					105					110			
Gly	Gln	Asp	Asn	Val	Met	Gly	Val	Lys	Tyr	Cys	Phe	Arg	Lys	Asn	Asp	
		115					120					125				
His	Val	Val	Ile	Ala	Met	Pro	Tyr	Leu	Glu	His	Glu	Ser	Phe	Leu	Asp	
	130					135					140					
Ile	Leu	Asn	Ser	Leu	Ser	Phe	Gln	Glu	Val	Arg	Glu	Tyr	Met	Leu	Asn	
145					150					155					160	
Leu	Phe	Lys	Ala	Leu	Lys	Arg	Ile	His	Gln	Phe	Gly	Ile	Val	His	Arg	
				165					170					175		
Asp	Val	Lys	Pro	Ser	Asn	Phe	Leu	Tyr	Asn	Arg	Arg	Leu	Lys	Lys	Tyr	
			180					185					190			
Ala	Leu	Val	Asp	Phe	Gly	Leu	Ala	Gln	Gly	Thr	His	Asp	Thr	Lys	Ile	
		195					200					205				
Glu	Leu	Leu	Lys	Phe	Val	Gln	Ser	Glu	Ala	Gln	Gln	Glu	Arg	Cys	Ser	
	210					215						220				
Gln	Asn	Lys	Ser	His	Ile	Ile	Thr	Gly	Asn	Lys	Ile	Pro	Leu	Ser	Gly	
225					230					235					240	
Pro	Val	Pro	Lys	Glu	Leu	Asp	Gln	Gln	Ser	Thr	Thr	Lys	Ala	Ser	Val	
				245					250					255		
Lys	Arg	Pro	Tyr	Thr	Asn	Ala	Gln	Ile	Gln	Ile	Lys	Gln	Gly	Lys	Asp	
			260					265					270			
Gly	Lys	Glu	Gly	Ser	Val	Gly	Leu	Ser	Val	Gln	Arg	Ser	Val	Phe	Gly	
		275					280					285				
Glu	Arg	Asn	Phe	Asn	Ile	His	Ser	Ser	Ile	Ser	His	Glu	Ser	Pro	Ala	
	290					295					300					
Val	Lys	Leu	Met	Lys	Gln	Ser	Lys	Thr	Val	Asp	Val	Leu	Ser	Arg	Lys	
305					310					315					320	
Leu	Ala	Thr	Lys	Lys	Lys	Ala	Ile	Ser	Thr	Lys	Val	Met	Asn	Ser	Ala	
				325					330					335		
Val	Met	Arg	Lys	Thr	Ala	Ser	Ser	Cys	Pro	Ala	Ser	Leu	Thr	Cys	Asp	
			340					345					350			
Cys	Tyr	Ala	Thr	Asp	Lys	Val	Cys	Ser	Ile	Cys	Leu	Ser	Arg	Arg	Gln	
		355					360					365				
Gln	Val	Ala	Pro	Arg	Ala	Gly	Thr	Pro	Gly	Phe	Arg	Ala	Pro	Glu	Val	
	370					375					380					

Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala
 385 390 395 400

Gly Val Ile Phe Leu Ser Leu Leu Ser
 405

<210> 41
 <211> 314
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> CDC7

<400> 41
 Met Thr Ser Lys Thr Lys Asn Ile Asp Asp Ile Pro Pro Glu Ile Lys
 1 5 10 15
 Glu Glu Met Ile Gln Leu Tyr His Asp Leu Pro Gly Ile Glu Asn Glu
 20 25 30
 Tyr Lys Leu Ile Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr
 35 40 45
 Lys Ala Lys Asp Ile Thr Gly Lys Ile Thr Lys Lys Phe Ala Ser His
 50 55 60
 Phe Trp Asn Tyr Gly Ser Asn Tyr Val Ala Leu Lys Lys Ile Tyr Val
 65 70 75 80
 Thr Ser Ser Pro Gln Arg Ile Tyr Asn Glu Leu Asn Leu Leu Tyr Ile
 85 90 95
 Met Thr Gly Ser Ser Arg Val Ala Pro Leu Cys Asp Ala Lys Arg Val
 100 105 110
 Arg Asp Gln Val Ile Ala Val Leu Pro Tyr Tyr Pro His Glu Glu Phe
 115 120 125
 Arg Thr Phe Tyr Arg Asp Leu Pro Ile Lys Gly Ile Lys Lys Tyr Ile
 130 135 140
 Trp Glu Leu Leu Arg Ala Leu Lys Phe Val His Ser Lys Gly Ile Ile
 145 150 155 160
 His Arg Asp Ile Lys Pro Thr Asn Phe Leu Phe Asn Leu Glu Leu Gly
 165 170 175
 Arg Gly Val Leu Val Asp Phe Gly Leu Ala Glu Ala Gln Met Asp Tyr
 180 185 190
 Lys Ser Met Ile Ser Ser Gln Asn Asp Tyr Asp Asn Tyr Ala Asn Thr
 195 200 205
 Asn His Asp Gly Gly Tyr Ser Met Arg Asn His Glu Gln Phe Cys Pro
 210 215 220
 Cys Ile Met Arg Asn Gln Tyr Ser Pro Asn Ser His Asn Gln Thr Pro
 225 230 235 240

Pro Met Val Thr Ile Gln Asn Gly Lys Val Val His Leu Asn Asn Val
245 250 255

Asn Gly Val Asp Leu Thr Lys Gly Tyr Pro Lys Asn Glu Thr Arg Arg
260 265 270

Ile Lys Arg Ala Asn Arg Ala Gly Thr Arg Gly Phe Arg Ala Pro Glu
275 280 285

Val Leu Met Lys Cys Gly Ala Gln Ser Thr Lys Ile Asp Ile Trp Ser
290 295 300

Val Gly Val Ile Leu Leu Ser Leu Leu Gly
305 310

<210> 42

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:protein kinase
consensus sequence

<400> 42

Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
1 5 10 15

Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
20 25 30

Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu
35 40 45

Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile
50 55 60

Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr
65 70 75 80

Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro
85 90 95

Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly
100 105 110

Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro
115 120 125

Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp
130 135 140

Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe
145 150 155 160

Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly
165 170 175

Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu
180 185 190

Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro
 195 200 205
 Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu
 210 215 220
 Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu
 225 230 235 240
 Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu
 245 250 255
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
 260 265 270
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
 275 280 285
 Leu Asn His Pro Trp Phe
 290

<210> 43
 <211> 253
 <212> PRT
 <213> Homo sapiens

<220>
 <223> cytokine-inducible kinase (CNK) serine threonine
 kinase, proliferation-related kinase (PRK),
 polo-like kinase 3 (PLK3)

<400> 43
 Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr
 1 5 10 15
 Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala Tyr Ala Val Lys Val Ile
 20 25 30
 Pro Gln Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Leu Asn
 35 40 45
 Glu Ile Glu Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe
 50 55 60
 Ser His His Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu
 65 70 75 80
 Cys Ser Arg Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu
 85 90 95
 Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu
 100 105 110
 Lys Tyr Leu His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly
 115 120 125
 Asn Phe Phe Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly
 130 135 140

Leu	Ala	Ala	Arg	Leu	Glu	Pro	Pro	Glu	Gln	Arg	Lys	Lys	Thr	Ile	Cys
145					150					155					160
Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val	Leu	Leu	Arg	Gln	Gly	His
			165						170					175	
Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Leu	Gly	Cys	Val	Met	Tyr	Thr	Leu
			180					185					190		
Leu	Cys	Gly	Ser	Pro	Pro	Phe	Glu	Thr	Ala	Asp	Leu	Lys	Glu	Thr	Tyr
		195					200					205			
Arg	Cys	Ile	Lys	Gln	Val	His	Tyr	Thr	Leu	Pro	Ala	Ser	Leu	Ser	Leu
	210					215					220				
Pro	Ala	Arg	Gln	Leu	Leu	Ala	Ala	Ile	Leu	Arg	Ala	Ser	Pro	Arg	Asp
225					230					235					240
Arg	Pro	Ser	Ile	Asp	Gln	Ile	Leu	Arg	His	Asp	Phe	Phe			
				245					250						

<210> 44
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus peptide

<400> 44
 His Arg Asp Leu Lys
 1 5

<210> 45
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus peptide

<400> 45
 Asp Phe Gly Leu Ala
 1 5

<210> 46
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus peptide

<400> 46
Ala Pro Glu Val
1

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 47
Asp Val Trp Ser Leu Gly
1 5

<210> 48
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine kinase 2 (STK2, NEK4)

<400> 48
Tyr Cys Tyr Leu Arg Val Val Gly Lys Gly Ser Tyr Gly Glu Val Thr
1 5 10 15
Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr Val Ile Lys Lys Leu
20 25 30
Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg Ala Ala Glu Gln Glu
35 40 45
Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn Ile Val Thr Tyr Lys
50 55 60
Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr Ile Val Met Gly Phe
65 70 75 80
Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys Glu Gln Lys Gly Gln
85 90 95
Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe Val Gln Ile Ala Met
100 105 110
Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu His Arg Asp Leu Lys
115 120 125
Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile Ile Lys Val Gly Asp
130 135 140
Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys Asp Met Ala Ser Thr
145 150 155 160
Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu Leu Phe Ser Asn Lys
165 170 175

Pro	Tyr	Asn	Tyr	Lys	Ser	Asp	Val	Trp	Ala	Leu	Gly	Cys	Cys	Val	Tyr
			180					185					190		
Glu	Met	Ala	Thr	Leu	Lys	His	Ala	Phe	Asn	Ala	Lys	Asp	Met	Asn	Ser
		195					200					205			
Leu	Val	Tyr	Arg	Ile	Ile	Glu	Gly	Lys	Leu	Pro	Pro	Met	Pro	Arg	Asp
	210					215					220				
Tyr	Ser	Pro	Glu	Leu	Ala	Glu	Leu	Ile	Arg	Thr	Met	Leu	Ser	Lys	Arg
225					230					235					240
Pro	Glu	Glu	Arg	Pro	Ser	Val	Arg	Ser	Ile	Leu	Arg	Gln	Pro	Tyr	Ile
				245					250						255

<210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 49
 His Pro Asn Ile Val
 1 5

<210> 50
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 50
 Glu Gly Gly Asp Leu
 1 5

<210> 51
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:protein kinase
 consensus sequence

<400> 51
 Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
 1 5 10 15
 Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
 20 25 30

Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu
 35 40 45
 Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile
 50 55 60
 Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr
 65 70 75 80
 Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro
 85 90 95
 Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly
 100 105 110
 Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro
 115 120 125
 Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp
 130 135 140
 Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe
 145 150 155 160
 Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly
 165 170 175
 Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu
 180 185 190
 Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro
 195 200 205
 Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu
 210 215 220
 Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu
 225 230 235 240
 Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu
 245 250 255
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
 260 265 270
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
 275 280 285
 Leu Asn His Pro Trp Phe
 290

<210> 52

<211> 286

<212> PRT

<213> Homo sapiens

<220>

<223> serine threonine protein kinase casein kinase 2,
 alpha 1 subunit isoform a, transcript variant 2
 (CK2, CK2alpha), CK2 catalytic subunit alpha

<400> 52

Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe
1 5 10 15
Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu
20 25 30
Lys Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu
35 40 45
Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys
50 55 60
Asp Pro Val Ser Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn
65 70 75 80
Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg
85 90 95
Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met
100 105 110
Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp His
115 120 125
Glu His Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr
130 135 140
His Pro Gly Gln Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys
145 150 155 160
Gly Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp
165 170 175
Met Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu
180 185 190
Pro Phe Phe His Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala
195 200 205
Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn
210 215 220
Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg
225 230 235 240
Lys Arg Trp Glu Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser
245 250 255
Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln
260 265 270
Ser Arg Leu Thr Ala Arg Glu Ala Met Glu His Pro Tyr Phe
275 280 285

<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 53
 Val Lys Ile Leu Lys
 1 5

<210> 54
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 54
 Trp Ser Leu Gly
 1

<210> 55
 <211> 298
 <212> PRT
 <213> Homo sapiens

<220>
 <223> cyclin-dependent kinase 2 (CDK2)

<400> 55
 Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1 5 10 15
 Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
 20 25 30
 Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
 35 40 45
 Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
 50 55 60
 Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
 65 70 75 80
 Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
 85 90 95
 Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
 100 105 110
 Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
 115 120 125
 Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
 130 135 140
 Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
 145 150 155 160

<210> 57
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flap structure-specific endonuclease 1 (FEN1)
 5'-3' exonuclease

<400> 57
 Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
 1 5 10 15
 Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
 20 25 30
 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35 40 45
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50 55 60
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65 70 75 80
 Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
 85 90 95
 Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala
 100 105

<210> 58
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 58
 Ala Ile Asp Ala Ser
 1 5

<210> 59
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 59
 Tyr Gln Phe Leu
 1

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 60
Asn Glu Glu Gly Glu Thr Thr Ser His Leu Met Gly
1 5 10

<210> 61
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 61
Gly Ile Lys Pro
1

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 62
Val Phe Asp Gly
1

<210> 63
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Xeroderma
pigmentosum complementation group XPG I-region
domain (XPG_I) consensus sequence

<400> 63
Arg Leu Met Gly Ile Pro Tyr Ile Val Ala Pro Gly Val Glu Ala Glu
1 5 10 15

Ala Gln Cys Ala Tyr Leu Glu Lys Lys Gly Leu Val Asp Gly Ile Ile
20 25 30

Thr Glu Asp Ser Asp Val Leu Leu Phe Gly Ala Pro Arg Leu Leu Arg
35 40 45

Asn Leu Thr Leu Ser Gly Lys Lys Ser Gly Pro Ser Ile Thr Ser Leu
 50 55 60
 Lys Val Glu Ile Glu Glu Ile Asp Leu Glu Ser Leu Leu Arg Glu Leu
 65 70 75 80
 Gly Leu Gly Lys Leu Ser Arg Glu Gln Leu Ile Asp Leu Ala Ile Leu
 85 90 95
 Leu Gly Cys Asp Tyr Thr Glu Gly
 100

<210> 64
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <223> flap structure-specific endonuclease 1 (FEN1)
 5'-3' exonuclease

<400> 64
 Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala
 1 5 10 15
 Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr
 20 25 30
 Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His
 35 40 45
 Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu
 50 55 60
 Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp
 65 70 75 80
 Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser
 85 90

<210> 65
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 peptide

<400> 65
 Leu Met Gly Ile Pro Tyr
 1 5

<210> 66
 <211> 4
 <212> PRT
 <213> Artificial Sequence

His Lys Thr Leu Tyr Tyr Asp Val Glu Pro Phe Leu Phe Tyr Val Met
 85 90 95
 Thr Glu Ala Asp Asn Thr Gly Cys His Leu Ile Gly Tyr Phe Ser Lys
 100 105 110
 Glu Lys Asn Ser Phe Leu Asn Tyr Asn Val Ser Cys Ile Leu Thr Met
 115 120 125
 Pro Gln Tyr Met Arg Gln Gly Tyr Gly Lys Met Leu Ile Asp Phe Ser
 130 135 140
 Tyr Leu Leu Ser Lys Val Glu Glu Lys Val Gly Ser Pro Glu Arg Pro
 145 150 155 160
 Leu Ser Asp Leu Gly Leu Ile Ser Tyr Arg Ser Tyr Trp Lys Glu Val
 165 170 175
 Leu Leu Arg Tyr Leu His Asn Phe Gln Gly Lys Glu Ile Ser Ile Lys
 180 185 190
 Glu Ile Ser Gln Glu Thr Ala Val Asn Pro Val Asp Ile Val Ser Thr
 195 200 205
 Leu Gln Ala Leu Gln Met Leu Lys Tyr Trp Lys Gly Lys His Leu Val
 210 215 220
 Leu Lys Arg Gln Asp Leu Ile Asp Glu Trp Ile Ala Lys Glu Ala Lys
 225 230 235 240
 Arg Ser Asn Ser Asn Lys Thr Met Asp Pro Ser Cys Leu Lys Trp Thr
 245 250 255
 Pro Pro Lys Gly Thr
 260

<210> 70
 <211> 265
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> Esal

<400> 70
 Tyr Phe Ser Pro Tyr Pro Ile Glu Leu Thr Asp Glu Asp Phe Ile Tyr
 1 5 10 15
 Ile Asp Asp Phe Thr Leu Gln Tyr Phe Gly Ser Lys Lys Gln Tyr Glu
 20 25 30
 Arg Tyr Arg Lys Lys Cys Thr Leu Arg His Pro Pro Gly Asn Glu Ile
 35 40 45
 Tyr Arg Asp Asp Tyr Val Ser Phe Phe Glu Ile Asp Gly Arg Lys Gln
 50 55 60
 Arg Thr Trp Cys Arg Asn Leu Cys Leu Leu Ser Lys Leu Phe Leu Asp
 65 70 75 80

His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Pro	Phe	Leu	Phe	Tyr	Cys	Met
				85					90					95	
Thr	Arg	Arg	Asp	Glu	Leu	Gly	His	His	Leu	Val	Gly	Tyr	Phe	Ser	Lys
			100					105					110		
Glu	Lys	Glu	Ser	Ala	Asp	Gly	Tyr	Asn	Val	Ala	Cys	Ile	Leu	Thr	Leu
		115					120					125			
Pro	Gln	Tyr	Gln	Arg	Met	Gly	Tyr	Gly	Lys	Leu	Leu	Ile	Glu	Phe	Ser
	130					135					140				
Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Asn	Lys	Val	Gly	Ser	Pro	Glu	Lys	Pro
145					150					155					160
Leu	Ser	Asp	Leu	Gly	Leu	Leu	Ser	Tyr	Arg	Ala	Tyr	Trp	Ser	Asp	Thr
				165					170					175	
Leu	Ile	Thr	Leu	Leu	Val	Glu	His	Gln	Lys	Glu	Ile	Thr	Ile	Asp	Glu
			180					185					190		
Ile	Ser	Ser	Met	Thr	Ser	Met	Thr	Thr	Thr	Asp	Ile	Leu	His	Thr	Ala
		195					200					205			
Lys	Thr	Leu	Asn	Ile	Leu	Arg	Tyr	Tyr	Lys	Gly	Gln	His	Ile	Ile	Phe
	210					215					220				
Leu	Asn	Glu	Asp	Ile	Leu	Asp	Arg	Tyr	Asn	Arg	Leu	Lys	Ala	Lys	Lys
225					230					235					240
Arg	Arg	Thr	Ile	Asp	Pro	Asn	Arg	Leu	Ile	Trp	Lys	Pro	Pro	Val	Phe
				245					250					255	
Thr	Ala	Ser	Gln	Leu	Arg	Phe	Ala	Trp							
			260					265							

<210> 71

<211> 253

<212> PRT

<213> Homo sapiens

<220>

<223> PIM1 oncogene serine threonine kinase

<400> 71

Tyr	Gln	Val	Gly	Pro	Leu	Leu	Gly	Ser	Gly	Gly	Phe	Gly	Ser	Val	Tyr
1				5					10					15	
Ser	Gly	Ile	Arg	Val	Ser	Asp	Asn	Leu	Pro	Val	Ala	Ile	Lys	His	Val
			20					25					30		
Glu	Lys	Asp	Arg	Ile	Ser	Asp	Trp	Gly	Glu	Leu	Pro	Asn	Gly	Thr	Arg
		35					40					45			
Val	Pro	Met	Glu	Val	Val	Leu	Leu	Lys	Lys	Val	Ser	Ser	Gly	Phe	Ser
	50					55					60				
Gly	Val	Ile	Arg	Leu	Leu	Asp	Trp	Phe	Glu	Arg	Pro	Asp	Ser	Phe	Val
65					70				75						80

Leu	Ile	Leu	Glu	Arg	Pro	Glu	Pro	Val	Gln	Asp	Leu	Phe	Asp	Phe	Ile
				85					90					95	
Thr	Glu	Arg	Gly	Ala	Leu	Gln	Glu	Glu	Leu	Ala	Arg	Ser	Phe	Phe	Trp
			100					105					110		
Gln	Val	Leu	Glu	Ala	Val	Arg	His	Cys	His	Asn	Cys	Gly	Val	Leu	His
		115					120					125			
Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Asn	Arg	Gly	Glu
	130					135					140				
Leu	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	Lys	Asp	Thr	Val
145					150					155					160
Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp	Ile
			165						170					175	
Arg	Tyr	His	Arg	Tyr	His	Gly	Arg	Ser	Ala	Ala	Val	Trp	Ser	Leu	Gly
			180					185					190		
Ile	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp	Ile	Pro	Phe	Glu	His	Asp
		195					200					205			
Glu	Glu	Ile	Ile	Arg	Gly	Gln	Val	Phe	Phe	Arg	Gln	Arg	Val	Ser	Ser
	210					215					220				
Glu	Cys	Gln	His	Leu	Ile	Arg	Trp	Cys	Leu	Ala	Leu	Arg	Pro	Ser	Asp
225					230					235					240
Arg	Pro	Thr	Phe	Glu	Glu	Ile	Gln	Asn	His	Pro	Trp	Met			
			245					250							

<210> 72

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 72

Asp Leu Phe Asp

1

<210> 73

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 73

Glu Asn Ile Leu

1

<210> 74
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 74
Val Trp Ser Leu Gly
1 5

<210> 75
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 75
Asn His Pro Trp
1

<210> 76
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'-end
32P-labeled oligonucleotide primer

<400> 76
cactgactgt atg

13

<210> 77
<211> 30
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA
Molecule:oligonucleotide template

<220>
<223> Description of Artificial Sequence:oligonucleotide
template

<400> 77
ctcgtcagca tcttcaucat acagtcagtg

30

<210> 78
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

<400> 78
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190
 Gly Gly Gly Gly Gly Gly Gly Gly
 195 200